

## SEQUENCE LISTING

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<120> A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE  
 RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF

<130> 6017.US.01

<140> 08/771,737  
 <141> 1996-12-20

<160> 8

<170> FastSEQ for Windows Version 3.0

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 <212> DNA  
 <213> homo sapien

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tct ctc ctg cac gtg tcc ctg caa ggc gag ttc cag agg aag ctt tac	98
Ser Leu Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr	
15                20                25                30	

aag gag ctg gtc aag aac tac aat ccc ttg gag agg ccc gtg gcc aat	146
Lys Glu Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn	
35                40                45	

gac tcg caa cca ctc acc gtc tac ttc tcc ctg agc ctc ctg cag atc	194
Asp Ser Gln Pro Leu Thr Val Tyr Ser Leu Ser Leu Gln Ile	
50                55                60	

atg gac gtg gat gag aag aac caa gtt tta acc acc aac att tgg ctg	242
Met Asp Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu	
65                70                75	

caa atg tct tgg aca gat cac tat tta cag tgg aat gtg tca gaa tat	290
Gln Met Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr	

80	85	90	
cca ggg gtg aag act gtt cgt ttc cca gat ggc cag att tgg aaa cca Pro Gly Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro	95	100	338
105			110
gac att ctt ctc tat aac agt gct gat gag cgc ttt gac gcc aca ttc Asp Ile Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe	115	120	386
125			
cac act aac gtg ttg gtg aat tct tct ggg cat tgc cag tac ctg cct His Thr Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro	130	135	434
140			
cca ggc ata ttc aag agt tcc tgc tac atc gat gta cgc tgg ttt ccc Pro Gly Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro	145	150	482
155			
ttt gat gtg cag cac tgc aaa ctg aag ttt ggg tcc tgg tct tac gga Phe Asp Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly	160	165	530
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ggc tgg tcc ttg gat ctg cag atg cag gag gca gat atc agt ggc tat Gly Trp Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr	175	180	578
185			190
atc ccc aat gga gaa tgg gac cta gtg gga atc ccc ggc aag agg agt Ile Pro Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser	195	200	626
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gaa agg ttc tat gag tgc tgc aaa gag ccc tac ccc gat gtc acc ttc Glu Arg Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe	210	215	674
220			
aca gtg acc atg cgc cgc agg aca ctc tac tat ggc ctc aac ctg ctg Thr Val Thr Met Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu	225	230	722
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atc ccc tgt gtg ctc atc tcc gcc ctc gcc ctg ctg gtg ttc ctg ctt Ile Pro Cys Val Leu Ile Ser Ala Leu Ala Leu Val Phe Leu Leu	240	245	770
250			
cct gca gat tcc ggg gag aag att tcc ctg ggg ata aca gtc tta ctc Pro Ala Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu	255	260	818
265			270
tct ctt acc acc ttc atg ctg ctc gtg gct gag atc atg ccc gca aca Ser Leu Thr Thr Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr	275	280	866
285			
tcc gat tcg gta cca ttg ata gcc cag tac ttc gcc agc acc atg atc Ser Asp Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile	290	295	914
300			
atc gtg ggc ctc tcg gtg gtg acg gtg atc gtg ctg cag tac cac Ile Val Gly Leu Ser Val Val Val Thr Val Ile Val Leu Gln Tyr His	305	310	962
315			

cac cac gac ccc gac ggc ggc aag atg ccc aag tgg acc aga gtc atc His His Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Val Ile 320 325 330	1010
ctt ctg aac tgg tgc gcg tgg ttc ctg cga atg aag agg ccc ggg gag Leu Leu Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu 335 340 345 350	1058
gac aag gtg cgc ccg gcc tgc cag cac aag cag ccg cgc tgc agc ctg Asp Lys Val Arg Pro Ala Cys Gln His Lys Gln Arg Arg Cys Ser Leu 355 360 365	1106
gcc agt gtg gag atg agc gcc gtg gcg ccg ccc gcc agc aac ggg Ala Ser Val Glu Met Ser Ala Val Ala Pro Pro Ala Ser Asn Gly 370 375 380	1154
aac ctg ctg tac atc ggc ttc cgc ggc ctg gac ggc gtg cac tgt gtc Asn Leu Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val 385 390 395	1202
ccg acc ccc gac tct ggg gta gtg tgt ggc cgc atg gcc tgc tcc ccc Pro Thr Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro 400 405 410	1250
acg cac gat gag cac ctc ctg cac ggc ggg caa ccc ccc gag ggg gac Thr His Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp 415 420 425 430	1298
ccg gac ttg gcc aag atc ctg gag gag gtc cgc tac att gcc aac cgc Pro Asp Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg 435 440 445	1346
ttc cgc tgc cag gac gaa agc gag gcg gtc tgc agc gag tgg aag ttc Phe Arg Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe 450 455 460	1394
gcc gcc tgt gtg gac cgc ctg tgc ctc atg gcc ttc tcg gtc ttc Ala Ala Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe 465 470 475	1442
acc atc atc tgc acc atc ggc atc ctg atg tcg gct ccc aac ttc gtg Thr Ile Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val 480 485 490	1490
gag gcc gtg tcc aaa gac ttt gcg taaccacgcc tgggtctgta catgtggaaa Glu Ala Val Ser Lys Asp Phe Ala 495 500	1544
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<212> PRT  
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Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu  
 1 5 10 15  
 Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu  
 20 25 30  
 Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser  
 35 40 45  
 Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Gln Ile Met Asp  
 50 55 60  
 Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met  
 65 70 75 80  
 Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly  
 85 90 95  
 Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile  
 100 105 110  
 Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr  
 115 120 125  
 Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly  
 130 135 140  
 Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp  
 145 150 155 160  
 Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Trp  
 165 170 175  
 Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro  
 180 185 190  
 Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg  
 195 200 205  
 Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val  
 210 215 220  
 Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu Ile Pro  
 225 230 235 240  
 Cys Val Leu Ile Ser Ala Leu Ala Leu Leu Val Phe Leu Leu Pro Ala  
 245 250 255  
 Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu Ser Leu  
 260 265 270  
 Thr Thr Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr Ser Asp  
 275 280 285  
 Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile Ile Val  
 290 295 300  
 Gly Leu Ser Val Val Val Thr Val Ile Val Leu Gln Tyr His His His  
 305 310 315 320  
 Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Val Ile Leu Leu  
 325 330 335  
 Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu Asp Lys  
 340 345 350  
 Val Arg Pro Ala Cys Gln His Lys Gln Arg Arg Cys Ser Leu Ala Ser  
 355 360 365  
 Val Glu Met Ser Ala Val Ala Pro Pro Pro Ala Ser Asn Gly Asn Leu  
 370 375 380  
 Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val Pro Thr  
 385 390 395 400  
 Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro Thr His  
 405 410 415  
 Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp Pro Asp  
 420 425 430  
 Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg Phe Arg  
 435 440 445  
 Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe Ala Ala

450	455	460
Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe Thr Ile		
465	470	475
Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val Glu Ala		
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Val Ser Lys Asp Phe Ala		
	500	

<210> 3  
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<210> 4  
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<p>&lt;400&gt; 4</p> <p>gcagcatgaa ggtggtaaga gag</p>	23
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<210> 5  
<211> 23  
<212> DNA  
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<p>&lt;400&gt; 5</p> <p>ctctcttacc accttcatgc tgc</p>	23
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<210> 6  
<211> 20  
<212> DNA  
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<p>&lt;400&gt; 6</p> <p>gtactgcagc acgatcacccg</p>	20
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<210> 7  
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<p>&lt;400&gt; 7</p> <p>cgagccccatg aggtgttagcc</p>	20
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<210> 8  
<211> 20  
<212> DNA  
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<p>&lt;400&gt; 8</p> <p>ccaggcattc ggagcttgcc</p>	20
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